WE CLAIM:

1.   A method for identifying the probability of a molecular interaction within a biological network comprising;

        (i) representing molecules as sets of conserved features;

        (ii) computing the attraction probabilities between said features; and

        (iv) using the computation of step (ii) to identify the

            probability of a molecular interaction within a biological network.

2.   A method for identifying the probability of protein interactions within a biological network comprising;

        (i) representing proteins as sets of conserved features;

        (ii) computing the attraction probabilities between said features; and

        (iv) using the computation of step (ii) to identify the

            probability of a molecular interaction within a biological network.

3.   A method for identifying the probability of protein interactions within a biological network comprising;

        (i) representing proteins as sets of conserved features;

        (ii) computing the attraction probabilities between said features;

        (iii) computing the attraction probabilities between proteins; and

        (iv) using the computation of step (ii) and step (iii) to identify the

        probability of a molecular interaction within a biological network.

4.   The method of claim 1, 2 or 3 further comprising computing the topology of a biological network wherein those networks displaying a more biologically realistic topology are assigned a greater probability.

5.   The method of claim 1, 2 or 3 wherein the conserved features are protein domains or motifs.

6.   The method of claim 1, 2 or 3 wherein the conserved features are nucleic acid molecule motifs.

7.   The method of claim 2 or 3 wherein the attraction probabilities between features is computed using equation 6, 14, or 16.

8.   The method of claim 2 wherein the attraction probabilities between proteins is accomplished using equation 5 or 17.

9.   The method of claim 1 wherein the identification of a probability of a molecular interaction within a biological network is accomplished using equation 1.

10.   The method of claim 2 or 3 wherein the identification of a probability of a protein interaction within a biological network is accomplished using equation 1.

11.   The method of claim 4 wherein the topology of a biological network is determined using equation 2, 3, 4 or 7.

12.   The method of claim 1 further comprising computing the posterior probabilities of interaction between a set of molecules.

13.   The method of claim 2 further comprising computing the posterior probabilities of interaction between a set of proteins.

14.   The method of claim 12 or 13 wherein a Markov Chain Monte Carlo technique is used to compute the posterior probabilities of interaction between a set of proteins.

15. The method of claim 12 or 13 wherein equation 1 is used to compute the posterior probabilities of interaction between a set of proteins.

16.   A screening method for identification of a compound capable of modifying the interaction between at least two proteins comprising:

  (i) identifying an interaction between at least two proteins using the method of claim 2 or 3 ;

  (ii) contacting said proteins identified in step (i) with a test compound;

  (iii) comparing the interaction of the proteins in the presence of the test compound with the interaction in the absence of the test compound;

wherein a difference in the interaction of the proteins in the presence of the test

compound as compared to the interaction in the absence of a test compound indicates

identification of a compound capable of modifying the interaction between proteins.

17.   A screening method for identification of a compound capable of

modifying the interaction between at least two molecules comprising:

(i)   identifying an interaction between at least molecules using the

method of claim 1 ;

(ii)   contacting said molecules identified in step (i) with a test

compound;

(iii)   comparing the interaction of the molecules in the presence of the

test compound with the interaction in the absence of the test compound;

wherein a difference in the interaction of the molecules in the presence of the test

compound as compared to the interaction in the absence of a test compound indicates

identification of a compound capable of modifying the interaction between molecules.